

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Schmidt, Robert R.
Miller, Philip
- (ii) TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE α - AND β -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Saliwanchik & Saliwanchik
 - (B) STREET: 2421 N.W. 41st Street, Suite A-1
 - (C) CITY: Gainesville
 - (D) STATE: Florida
 - (E) COUNTRY: USA
 - (F) ZIP: 32606-6669
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/070,844
 - (B) FILING DATE: 01-MAY-98
- (viii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/725,596
 - (B) FILING DATE: 03-OCT-96

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/541,033
- (B) FILING DATE: 06-OCT-95

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lloyd, Jeff
- (B) REGISTRATION NUMBER: 35,589
- (C) REFERENCE/DOCKET NUMBER: UF-155CD3

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (352) 375-8100
- (B) TELEFAX: (352) 372-5800

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCTTTCTG CTCGCCCTCT CTCCGTCCCG CC ATG CAG ACC GCC CTC GTC GCC	53
Met Gln Thr Ala Leu Val Ala	
1 5	
AAG CCT ATC GTG GCC GCC CCG CTG GCG GCA CGC CCG CGC TGC CTC GCG	101
Lys Pro Ile Val Ala Ala Pro Leu Ala Ala Arg Pro Arg Cys Leu Ala	
10 15 20	

CCG TGG CCG TGC GCG TGG GTC CGC TCC GCC AAG CGC GAT GTC CGC GCC	149
Pro Trp Pro Cys Ala Trp Val Arg Ser Ala Lys Arg Asp Val Arg Ala	
25 30 35	
AAG GCC GTC TCG CTG GAG GAG CAG ATC TCC GCG ATG GAC GCC ACC ACC	197
Lys Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr Thr	
40 45 50 55	
GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG AAG CAG ATG GCC ACC AAG	245
Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala Thr Lys	
60 65 70	
GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC AAG AAC CCC GAC GTG CGC	293
Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp Val Arg	
75 80 85	
CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC CCG GAG CAG CAG GAG TTC	341
Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln Glu Phe	
90 95 100	
ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC CTG CAG CCC GTG TTC GAG	389
Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val Phe Glu	
105 110 115	
AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG CAG ATC GTT GAG CCT GAG	437
Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu Pro Glu	
120 125 130 135	
CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG GAC GAC GCC GGC AAC CTG	485
Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly Asn Leu	
140 145 150	
CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC TCG TCC GCC ATC GGC CCC	533
Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile Gly Pro	
155 160 165	
TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC GTG AAC CTG TCC ATC ATG	581
Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile Met	
170 175 180	

AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG AAC AGC CTG ACC ACC CTG	629
Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr Thr Leu	
185 190 195	
CCC ATG GGC GGC GGC AAG GGC GGC TCC GAC TTC GAC CCC AAG GGC AAG	677
Pro Met Gly Gly Gly Lys Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys	
200 205 210 215	
AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG TCC TTC ATG ACC GAG CTG	725
Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr Glu Leu	
220 225 230	
CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG CCC GCC GGC GAC ATC GGC	773
Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp Ile Gly	
235 240 245	
GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC GGC CAG TAC AAG CGC ATC	821
Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys Arg Ile	
250 255 260	
ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG AAG GGC CAG GAG TAT GGC	869
Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu Tyr Gly	
265 270 275	
GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC TAC GGC GCC GTG CTG TTT	917
Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val Leu Phe	
280 285 290 295	
GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG AGC CTC AAG GGC AAG CGC	965
Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly Lys Arg	
300 305 310	
TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC CAG TAC TGC GCG GAG CTG	1013
Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala Glu Leu	
315 320 325	
CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG CTG TCC GAC TCC CAG GGC	1061
Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser Gln Gly	
330 335 340	

TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC GAG CAG CTG CAG GCG GTG	1109
Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln Ala Val	
345 350 355	
 CAG GAC ATG AAG AAG AAG AAC AAC AGC GCC CGC ATC TCC GAG TAC AAG	1157
Gln Asp Met Lys Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu Tyr Lys	
360 365 370 375	
 AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC CGC AAG CCT TGG GAG CTG	1205
Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp Glu Leu	
380 385 390	
 GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC GCC ACC CAG AAC GAG ATC	1253
Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn Glu Ile	
395 400 405	
 GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG CAC GGC TGC CAG TAC GTG	1301
Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln Tyr Val	
410 415 420	
 GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC GAG GCC ATC CAC AAG TAC	1349
Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His Lys Tyr	
425 430 435	
 AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC AAG GCG GCC AAC GCC GGC	1397
Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn Ala Gly	
440 445 450 455	
 GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC CAG AAC CGC ATG AGC CTG	1445
Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met Ser Leu	
460 465 470	
 AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG CTG GAG CGC ATC ATG AAG	1493
Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile Met Lys	
475 480 485	

GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC CGC AGA TAC AAT GTT GAC	1541
Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn Val Asp	
490 495 500	
CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC ACC AAG GTG GCT GAT GCC	1589
Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala Asp Ala	
505 510 515	
GTC AAG GCC CAG GGC GCT GTT TAAGCTGCCC AGGCCCAAGC CACGGCTCAC	1640
Val Lys Ala Gln Gly Ala Val	
520 525	
CGGCAATCCA ACCCAACCAA CTCAACGGCC AGGACCTTTT CGGAAGCGGC GCCTTTTTTCC	1700
CAGCCAGGGC CCTCACCTGC CCTTTCATAA CCCTGCTATT GCCGCCGTGC CCCTGCAATT	1760
CCACCCCAAG AAGAACTAGC GGCAC TTGAC TGCATCAGGA CGGCTATTTT TTTCGCGACG	1820
CGCGCTCACC CCGAGAGCCT CTCTCCCCCG AGCCCTAAGC GCTGACGTCC GCCCGACTTT	1880
GCCTCGCACA TCGCTCGGTT TTGACCCCCT CCAGTCTACC CACCCTGTTG TGAAGCCTAC	1940
CAGCTCAATT GCCTTTTAGT GTATGTGCGC CCCCTCCTGC CCCC GAATTT TCCTGCCATG	2000
AGACGTGCGG TTCCTAGCCT GGTGACCCCA AGTAGCAGTT AGTGTGCGTG CCTTGCCCTG	2060
CGCTGCCCCG GATGCGATAC TGTGACCTGA GAGTGCTTGT GTAAACACGA CGAGTCAAAA	2120
AAAAAAAAA AAAAAAAAAA	2140

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Thr Ala Leu Val Ala Lys Pro Ile Val Ala Ala Pro Leu Ala
 1 5 10 15
 Ala Arg Pro Arg Cys Leu Ala Pro Trp Pro Cys Ala Trp Val Arg Ser
 20 25 30
 Ala Lys Arg Asp Val Arg Ala Lys Ala Val Ser Leu Glu Glu Gln Ile
 35 40 45
 Ser Ala Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala
 50 55 60
 Val Lys Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly
 65 70 75 80
 Ile Lys Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys
 85 90 95
 Asp Pro Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val Ala Val
 100 105 110
 Ser Leu Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe
 115 120 125
 Lys Gln Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp
 130 135 140
 Leu Asp Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln
 145 150 155 160
 Tyr Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro
 165 170 175
 Ser Val Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe
 180 185 190
 Lys Asn Ser Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly Gly Ser

195	200	205
Asp Phe Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys		
210	215	220
Gln Ser Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp		
225	230	235
Val Pro Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu		
245	250	255
Phe Gly Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr		
260	265	270
Pro Lys Gly Gln Glu Tyr Gly Gly Ser Glu Ile Arg Pro Glu Ala Thr		
275	280	285
Gly Tyr Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly		
290	295	300
Glu Ser Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val		
305	310	315
Ala Gln Tyr Cys Ala Glu Leu Leu Leu Glu Lys Gly Ala Ile Val Leu		
325	330	335
Ser Leu Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr		
340	345	350
Arg Glu Gln Leu Gln Ala Val Gln Asp Met Lys Lys Lys Asn Asn Ser		
355	360	365
Ala Arg Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp		
370	375	380
Arg Arg Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro		
385	390	395
Cys Ala Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile		
		400

405	410	415
Lys His Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr		
420	425	430
Asn Glu Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro		
435	440	445
Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met		
450	455	460
Thr Gln Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp		
465	470	475
Lys Leu Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro		
485	490	495
Ser Arg Arg Tyr Asn Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly		
500	505	510
Phe Thr Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val		
515	520	525

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..1568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCCTTTCTG CTCGCCCTCT CTCCGTCCCG CC ATG CAG ACC GCC CTC GTC GCC 53
 Met Gln Thr Ala Leu Val Ala
 1 5

AAG CCT ATC GTG GCC TGC GCG TGG GTC CGC TCC GCC AAG CGC GAT GTC 101
 Lys Pro Ile Val Ala Cys Ala Trp Val Arg Ser Ala Lys Arg Asp Val
 10 15 20

CGC GCC AAG GCC GTC TCG CTG GAG GAG CAG ATC TCC GCG ATG GAC GCC 149
 Arg Ala Lys Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala
 25 30 35

ACC ACC GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG AAG CAG ATG GCC 197
 Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala
 40 45 50 55

ACC AAG GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC AAG AAC CCC GAC 245
 Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp
 60 65 70

GTG CGC CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC CCG GAG CAG CAG 293
 Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln
 75 80 85

GAG TTC ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC CTG CAG CCC GTG 341
 Glu Phe Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val
 90 95 100

TTC GAG AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG CAG ATC GTT GAG 389
 Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu
 105 110 115

CCT GAG CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG GAC GAC GCC GGC 437
 Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly
 120 125 130 135

AAC CTG CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC TCG TCC GCC ATC 485
 Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile
 140 145 150

GGC CCC TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC GTG AAC CTG TCC	533
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser	
155 160 165	
ATC ATG AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG AAC AGC CTG ACC	581
Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr	
170 175 180	
ACC CTG CCC ATG GGC GGC GGC AAG GGC GGC TCC GAC TTC GAC CCC AAG	629
Thr Leu Pro Met Gly Gly Gly Lys Gly Gly Ser Asp Phe Asp Pro Lys	
185 190 195	
GGC AAG AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG TCC TTC ATG ACC	677
Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr	
200 205 210 215	
GAG CTG CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG CCC GCC GGC GAC	725
Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp	
220 225 230	
ATC GGC GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC GGC CAG TAC AAG	773
Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys	
235 240 245	
CGC ATC ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG AAG GGC CAG GAG	821
Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu	
250 255 260	
TAT GGC GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC TAC GGC GCC GTG	869
Tyr Gly Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val	
265 270 275	
CTG TTT GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG AGC CTC AAG GGC	917
Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly	
280 285 290 295	
AAG CGC TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC CAG TAC TGC GCG	965
Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala	
300 305 310	

GAG CTG CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG CTG TCC GAC TCC	1013
Glu Leu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser	
315 320 325	
CAG GGC TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC GAG CAG CTG CAG	1061
Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln	
330 335 340	
GCG GTG CAG GAC ATG AAG AAG AAG AAC AAC AGC GCC CGC ATC TCC GAG	1109
Ala Val Gln Asp Met Lys Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu	
345 350 355	
TAC AAG AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC CGC AAG CCT TGG	1157
Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp	
360 365 370 375	
GAG CTG GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC GCC ACC CAG AAC	1205
Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn	
380 385 390	
GAG ATC GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG CAC GGC TGC CAG	1253
Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln	
395 400 405	
TAC GTG GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC GAG GCC ATC CAC	1301
Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His	
410 415 420	
AAG TAC AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC AAG GCG GCC AAC	1349
Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn	
425 430 435	
GCC GGC GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC CAG AAC CGC ATG	1397
Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met	
440 445 450 455	
AGC CTG AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG CTG GAG CGC ATC	1445
Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile	
460 465 470	

ATG AAG GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC CGC AGA TAC AAT	1493
Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn	
475 480 485	
GTT GAC CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC ACC AAG GTG GCT	1541
Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala	
490 495 500	
GAT GCC GTC AAG GCC CAG GGC GCT GTT TAAGCTGCCC AGGCCCAAGC	1588
Asp Ala Val Lys Ala Gln Gly Ala Val	
505 510	
CACGGCTCAC CGGCAATCCA ACCCAACCAA CTCAACGGCC AGGACCTTTT CGGAAGCGGC	1648
GCCTTTTTTCC CAGCCAGGGC CCTCACCTGC CCTTTCATAA CCCTGCTATT GCCGCCGTGC	1708
CCCTGCAATT CCACCCCAAG AAGAACTAGC GGCAC TTGAC TGCATCAGGA CGGCTATTTT	1768
TTTCGCGACG CGCGCTCACC CCGAGAGCCT CTCTCCCCCG AGCCCTAAGC GCTGACGTCC	1828
GCCCGACTTT GCCTCGCACA TCGCTCGGTT TTGACCCCT CCAGTCTACC CACCCTGTTG	1888
TGAAGCCTAC CAGCTCAATT GCCTTTTAGT GTATGTGCGC CCCCTCCTGC CCCC GAATTT	1948
TCCTGCCATG AGACGTGCGG TTCCTAGCCT GGTGACCCCA AGTAGCAGTT AGTGTGCGTG	2008
CCTTGCCCTG CGCTGCCCCG GATGCGATAC TGTGACCTGA GAGTGCTTGT GTAAACACGA	2068
CGAGTCAAAA AAAAAAAAAA AAAAAAAAAA A	2099

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gln Thr Ala Leu Val Ala Lys Pro Ile Val Ala Cys Ala Trp Val
 1 5 10 15
 Arg Ser Ala Lys Arg Asp Val Arg Ala Lys Ala Val Ser Leu Glu Glu
 20 25 30
 Gln Ile Ser Ala Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln
 35 40 45
 Lys Ala Val Lys Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val
 50 55 60
 His Gly Ile Lys Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe
 65 70 75 80
 Met Lys Asp Pro Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val
 85 90 95
 Ala Val Ser Leu Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro
 100 105 110
 Ile Phe Lys Gln Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val
 115 120 125
 Ser Trp Leu Asp Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg
 130 135 140
 Val Gln Tyr Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe
 145 150 155 160
 His Pro Ser Val Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln
 165 170 175
 Ile Phe Lys Asn Ser Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly
 180 185 190
 Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg

195	200	205
Phe Cys Gln Ser Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val		
210	215	220
Gln Asp Val Pro Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly		
225	230	235 240
Tyr Leu Phe Gly Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val		
245	250	255
Leu Thr Pro Lys Gly Gln Glu Tyr Gly Gly Ser Glu Ile Arg Pro Glu		
260	265	270
Ala Thr Gly Tyr Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp		
275	280	285
Lys Gly Glu Ser Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly		
290	295	300
Asn Val Ala Gln Tyr Cys Ala Glu Leu Leu Leu Glu Lys Gly Ala Ile		
305	310	315 320
Val Leu Ser Leu Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly		
325	330	335
Phe Thr Arg Glu Gln Leu Gln Ala Val Gln Asp Met Lys Lys Lys Asn		
340	345	350
Asn Ser Ala Arg Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val		
355	360	365
Gly Asp Arg Arg Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala		
370	375	380
Phe Pro Cys Ala Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu		
385	390	395 400
Leu Ile Lys His Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro		

Asp Phe Thr Ala

20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp	Ala	Thr	Thr	Gly	Asp	Phe	Thr	Ala	Leu
1				5					10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1969 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGATCTCCG CGATGGACGC CACCACCGGC GACTTCACGG CGCTGCAGAA GGCGGTGAAG	60
CAGATGGCCA CCAAGGCGGG CACTGAGGGC CTGGTGCACG GCATCAAGAA CCCCACGTG	120
CGCCAGCTGC TGACCGAGAT CTTTCATGAAG GACCCGGAGC AGCAGGAGTT CATGCAGGCG	180

GTGCGCGAGG TGGCCGTCTC CCTGCAGCCC GTGTTTCGAGA AGCGCCCCGA GCTGCTGCCC	240
ATCTTCAAGC AGATCGTTGA GCCTGAGCGC GTGATCACCT TCCGCGTGTC CTGGCTGGAC	300
GACGCCGGCA ACCTGCAGGT CAACCGCGGC TTCCGCGTGC AGTACTCGTC CGCCATCGGC	360
CCCTACAAGG GCGGCCTGCG CTTCCACCCC TCCGTGAACC TGTCCATCAT GAAGTTCCTT	420
GCCTTTGAGC AGATCTTCAA GAACAGCCTG ACCACCCTGC CCATGGGCGG CGGCAAGGGC	480
GGCTCCGACT TCGACCCCAA GGGCAAGAGC GACGCGGAGG TGATGCGCTT CTGCCAGTCC	540
TTCATGACCG AGCTGCAGCG CCACATCAGC TACGTGCAGG ACGTGCCCGC CGGCGACATC	600
GGCGTGGGCG CGCGCGAGAT TGGCTACCTT TTCGGCCAGT ACAAGCGCAT CACCAAGAAC	660
TACACCGGCG TGCTGACCCC GAAGGGCCAG GAGTATGGCG GCTCCGAGAT CCGCCCCGAG	720
GCCACCGGCT ACGGCGCCGT GCTGTTTGTG GAGAACGTGC TGAAGGACAA GGGCGAGAGC	780
CTCAAGGGCA AGCGCTGCCT GGTGTCTGGC GCGGGCAACG TGGCCCAGTA CTGCGCGGAG	840
CTGCTGCTGG AGAAGGGCGC CATCGTGCTG TCGCTGTCCG ACTCCCAGGG CTACGTGTAC	900
GAGCCCAACG GCTTCACGCG CGAGCAGCTG CAGGCGGTGC AGGACATGAA GAAGAAGAAC	960
AACAGCGCCC GCATCTCCGA GTACAAGAGC GACACCGCCG TGTATGTGGG CGACCGCCGC	1020
AAGCCTTGGG AGCTGGACTG CCAGGTGGAC ATCGCCTTCC CCTGCGCCAC CCAGAACGAG	1080
ATCGATGAGC ACGACGCCGA GCTGCTGATC AAGCACGGCT GCCAGTACGT GGTGGAGGGC	1140
GCCAACATGC CCTCCACCAA CGAGGCCATC CACAAGTACA ACAAGGCCGG CATCATCTAC	1200
TGCCCCGGCA AGGCGGCCAA CGCCGGCGGC GTGGCGGTCA GCGGCCTGGA GATGACCCAG	1260
AACCGCATGA GCCTGAACTG GACTCGCGAG GAGGTTCGCG ACAAGCTGGA GCGCATCATG	1320
AAGGACATCT ACGACTCCGC CATGGGGCCG TCCCGCAGAT ACAATGTTGA CCTGGCTGCG	1380

GGCGCCAACA TCGCGGGCTT CACCAAGGTG GCTGATGCCG TCAAGGCCCA GGGCGCTGTT	1440
TAAGCTGCCC AGGCCCAAGC CACGGCTCAC CGGCAATCCA ACCCAACCAA CTCAACGGCC	1500
AGGACCTTTT CGGAAGCGGC GCCTTTTTTCC CAGCCAGGGC CCTCACCTGC CCTTTCATAA	1560
CCCTGCTATT GCCGCCGTGC CCCTGCAATT CCACCCCAAG AAGAACTAGC GGCACCTGAC	1620
TGCATCAGGA CGGCTATTTT TTTCGCGACG CGCGCTCACC CCGAGAGCCT CTCTCCCCCG	1680
AGCCCTAAGC GCTGACGTCC GCCCCGACTTT GCCTCGCACA TCGCTCGGTT TTGACCCCTT	1740
CCAGTCTACC CACCCTGTTG TGAAGCCTAC CAGCTCAATT GCCTTTTAGT GTATGTGCGC	1800
CCCCTCCTGC CCCCGAATTT TCCTGCCATG AGACGTGCGG TTCCTAGCCT GGTGACCCCA	1860
AGTAGCAGTT AGTGTGCGTG CCTTGCCCTG CGCTGCCCCG GATGCGATAC TGTGACCTGA	1920
GAGTGCTTGT GTAAACACGA CGAGTCAAAA AAAAAAAAAA AAAAAAAAAA	1969

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCAAAGGCA AGGAACTTCA TG

22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCGACAT TCTAGACAGA ATTCGTGGAT CCTTTTTTTTTT TTTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGACGAGTAC TGCACGC

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTCGGTC AGCAGCTG

18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCGACAT TCTAGACAGA A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGTCGACAT TCTAGACAGA ATTCGTGGAT CCTTTTTTTTTT TTTTTTTTTTTT TTTTTTCTCC	60
TTTCTGCTCG CCCTCTCTCC GTCCCGCCAT GCAGACCGCC CTCGTGCGCA AGCCTATCGT	120
GGCCGCCCCG CTGGCGGCAC GCCCGCGCTG CCTCGCGCCG TGGCCGTGCG CGTGGGTCCG	180
CTCCGCCAAG CGCGATGTCC GCGCCAAGGC CGTCTCGCTG GAGGAGCAGA TCTCCGCGAT	240
GGACGCCACC ACCGGCGACT TCACGGCGCT GCAGAAGGCG GTGAAGCAGA TGGCCACCAA	300
GGCGGGCACT GAGGGCCTGG TGCACGGCAT CAAGAACCCC GACGTGCGCC AGCTGCTGAC	360

CGAGATC

367

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGGTCGACAT TCTAGACAGA ATTCGTGGAT CCTTTTTTTTTT TTTTTTTTTTTT TTTTTTCTCC	60
TTTCTGCTCG CCCTCTCTCC GTCCCGCCAT GCAGACCGCC CTCGTCGCCA AGCCTATCGT	120
GGCCTGCGCG TGGGTCCGCT CCGCCAAGCG CGATGTCCGC GCCAAGGCCG TCTCGCTGGA	180
GGAGCAGATC TCCGCGATGG ACGCCACCAC CGGCGACTTC ACGGCGCTGC AGAAGGCGGT	240
GAAGCAGATG GCCACCAAGG CGGGCACTGA GGGCCTGGTG CACGGCATCA AGAACCCCGA	300
CGTGCGCCAG CTGCTGACCG AGATC	325

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTTCTGCTC GCCCTCTC

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCGCCCC GCTGGCGGCA CGCCCGCGCT GCCTCGCGCC GTGGCCGTGC GCGTGGGTCC	120
GCTCCGCCAA GCGCGATGTC CGCGCCAAGG CCGTCTCGCT GGAGGAGCAG ATCTCCGCGA	180
TGGACGCCAC CACCGGCGAC TTCACGGCGC TGCAGAAGGC GGTGAAGCAG ATGGCCACCA	240
AGGCGGGCAC TGAGGGCCTG GTGCACGGCA TCAAGAACCC CGACGTGCGC CAGCTGCTGA	300
CCGAGATC	308

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCTGCGC GTGGGTCCGC TCCGCCAAGC GCGATGTCCG CGCCAAGGCC GTCTCGCTGG	120
AGGAGCAGAT CTCCGCGATG GACGCCACCA CCGGCGACTT CACGGCGCTG CAGAAGGCGG	180
TGAAGCAGAT GGCCACCAAG GCGGGCACTG AGGGCCTGGT GCACGGCATC AAGAACCCCG	240
ACGTGCGCCA GCTGCTGACC GAGATC	266

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCGCCCC GCTGGCGGCA CGCCGCGCT GCCTCGCGCC GTGGCCGTGC GCGTGGGTCC	120
GCTCCGCCAA GCGCGATGTC CGCGCAAGG CCGTCTCGCT GGAGGAGCAG ATCTCCGCGA	180
TGGACGCCAC CACCGGCGAC TTCACGGCGC TGCAGAAGGC GGTGAAGCAG ATGGCCACCA	240
AGGCGGGCAC TGAGGGCCTG GTGCACGGCA TCAAGAACCC CGACGTGCGC CAGCTGCTGA	300
CCGAGATCTT CATGAAGGAC CCGGAGCAGC AGGAGTTCAT GCAGGCGGTG CGCGAGGTGG	360
CCGTCTCCCT GCAGCCCGTG TTCGAGAAGC GCCCCGAGCT GCTGCCCATC TTCAAGCAGA	420
TCGTTGAGCC TGAGCGCGTG ATCACCTTCC GCGTGTCTTG GCTGGACGAC GCCGGCAACC	480

TGCAGGTCAA CCGCGGCTTC CGCGTGCAGT ACTCGTCCGC CATCGGCCCC TACAAGGGCG	540
GCCTGCGCTT CCACCCCTCC GTGAACCTGT CCATCATGAA GTTCCTTGCC TTTGAGCAGA	600
TCTTCAAGAA CAGCCTGACC ACCCTGCCCA TGGGCGGCGG CAAGGGCGGC TCCGACTTCG	660
ACCCAAGGG CAAGAGCGAC GCGGAGGTGA TGCCTTCTG CCAGTCCTTC ATGACCGAGC	720
TGCAGCGCCA CATCAGCTAC GTGCAGGACG TGCCCGCCGG CGACATCGGC GTGGGCGCGC	780
GCGAGATTGG CTACCTTTTC GGCCAGTACA AGCGCATCAC CAAGAACTAC ACCGGCGTGC	840
TGACCCCGAA GGGCCAGGAG TATGGCGGCT CCGAGATCCG CCCCAGAGCC ACCGGCTACG	900
GCGCCGTGCT GTTTGTGGAG AACGTGCTGA AGGACAAGGG CGAGAGCCTC AAGGGCAAGC	960
GCTGCCTGGT GTCTGGCGCG GGCAACGTGG CCCAGTACTG CGCGGAGCTG CTGCTGGAGA	1020
AGGGCGCCAT CGTGCTGTCTG CTGTCCGACT CCCAGGGCTA CGTGTACGAG CCCAACGGCT	1080
TCACGCGCGA GCAGCTGCAG GCGGTGCAGG ACATGAAGAA GAAGAACAAC AGCGCCCGCA	1140
TCTCCGAGTA CAAGAGCGAC ACCGCCGTGT ATGTGGGCGA CCGCCGCAAG CCTTGGGAGC	1200
TGGA CTGCCA GGTGGACATC GCCTTCCCCT GCGCCACCCA GAACGAGATC GATGAGCACG	1260
ACGCCGAGCT GCTGATCAAG CACGGCTGCC AGTACGTGGT GGAGGGCGCC AACATGCCCT	1320
CCACCAACGA GGCCATCCAC AAGTACAACA AGGCCGGCAT CATCTACTGC CCCGGCAAGG	1380
CGGCCAACGC CGGCGGCGTG GCGGTCAGCG GCCTGGAGAT GACCCAGAAC CGCATGAGCC	1440
TGAACTGGAC TCGCGAGGAG GTTCGCGACA AGCTGGAGCG CATCATGAAG GACATCTACG	1500
ACTCCGCCAT GGGGCCGTCC CGCAGATACA ATGTTGACCT GGCTGCGGGC GCCAACATCG	1560
CGGGCTTCAC CAAGGTGGCT GATGCCGTCA AGGCCAGGG CGCTGTTTAA GCTGCCCAGG	1620
CCCAAGCCAC GGCTCACCGG CAATCCAACC CAACCAACTC AACGGCCAGG ACCTTTTCGG	1680

AAGCGGCGCC TTTTCCCAG CCAGGGCCCT CACCTGCCCT TTCATAACCC TGCTATTGCC	1740
GCCGTGCCCC TGCAATTCCA CCCCAAGAAG AACTAGCGGC ACTTGACTGC ATCAGGACGG	1800
CTATTTTTTTT CGCGACGCGC GCTCACCCCG AGAGCCTCTC TCCCCGAGC CCTAAGCGCT	1860
GACGTCCGCC CGACTTTGCC TCGCACATCG CTCGGTTTTG ACCCCCTCCA GTCTACCCAC	1920
CCTGTTGTGA AGCCTACCAG CTCAATTGCC TTTTAGTGTA TGTGCGCCCC CTCCTGCCCC	1980
CGAATTTTCC TGCCATGAGA CGTGCGGTTT CTAGCCTGGT GACCCCAAGT AGCAGTTAGT	2040
GTGCGTGCCT TGCCCTGCGC TGCCCGGGAT GCGATACTGT GACCTGAGAG TGCTTGTGTA	2100
AACACGACGA GTCAAAAAA AAAAAAAAAA AAAAAA	2137

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCTGCGC GTGGGTCCGC TCCGCCAAGC GCGATGTCCG CGCCAAGGCC GTCTCGCTGG	120
AGGAGCAGAT CTCCGCGATG GACGCCACCA CCGGCGACTT CACGGCGCTG CAGAAGGCGG	180
TGAAGCAGAT GGCCACCAAG GCGGGCACTG AGGGCCTGGT GCACGGCATC AAGAACCCCG	240
ACGTGCGCCA GCTGCTGACC GAGATCTTCA TGAAGGACCC GGAGCAGCAG GAGTTCATGC	300

AGGCGGTGCG	CGAGGTGGCC	GTCTCCCTGC	AGCCCGTGTT	CGAGAAGCGC	CCCAGACTGC	360
TGCCCATCTT	CAAGCAGATC	GTTGAGCCTG	AGCGCGTGAT	CACCTTCCGC	GTGTCCTGGC	420
TGGACGACGC	CGGCAACCTG	CAGGTCAACC	GCGGCTTCCG	CGTGCAGTAC	TCGTCCGCCA	480
TCGGCCCCTA	CAAGGGCGGC	CTGCGCTTCC	ACCCCTCCGT	GAACCTGTCC	ATCATGAAGT	540
TCCTTGCCCT	TGAGCAGATC	TTCAAGAACA	GCCTGACCAC	CCTGCCCATG	GGCGGCGGCA	600
AGGGCGGCTC	CGACTTCGAC	CCCAAGGGCA	AGAGCGACGC	GGAGGTGATG	CGCTTCTGCC	660
AGTCCTTCAT	GACCGAGCTG	CAGCGCCACA	TCAGCTACGT	GCAGGACGTG	CCCGCCGGCG	720
ACATCGGCGT	GGGCGCGCGC	GAGATTGGCT	ACCTTTTCGG	CCAGTACAAG	CGCATCACCA	780
AGAACTACAC	CGGCGTGCTG	ACCCCGAAGG	GCCAGGAGTA	TGGCGGCTCC	GAGATCCGCC	840
CCGAGGCCAC	CGGCTACGGC	GCCGTGCTGT	TTGTGGAGAA	CGTGCTGAAG	GACAAGGGCG	900
AGAGCCTCAA	GGGCAAGCGC	TGCCTGGTGT	CTGGCGCGGG	CAACGTGGCC	CAGTACTGCG	960
CGGAGCTGCT	GCTGGAGAAG	GGCGCCATCG	TGCTGTCGCT	GTCCGACTCC	CAGGGCTACG	1020
TGTACGAGCC	CAACGGCTTC	ACGCGCGAGC	AGCTGCAGGC	GGTGCAGGAC	ATGAAGAAGA	1080
AGAACAACAG	CGCCCGCATC	TCCGAGTACA	AGAGCGACAC	CGCCGTGTAT	GTGGGCGACC	1140
GCCGCAAGCC	TTGGGAGCTG	GACTGCCAGG	TGGACATCGC	CTTCCCCTGC	GCCACCCAGA	1200
ACGAGATCGA	TGAGCACGAC	GCCGAGCTGC	TGATCAAGCA	CGGCTGCCAG	TACGTGGTGG	1260
AGGGCGCCAA	CATGCCCTCC	ACCAACGAGG	CCATCCACAA	GTACAACAAG	GCCGGCATCA	1320
TCTACTGCCC	CGGCAAGGCG	GCCAACGCCG	GCGGCGTGGC	GGTCAGCGGC	CTGGAGATGA	1380
CCCAGAACCG	CATGAGCCTG	AACTGGACTC	GCGAGGAGGT	TCGCGACAAG	CTGGAGCGCA	1440
TCATGAAGGA	CATCTACGAC	TCCGCCATGG	GGCCGTCCCG	CAGATACAAT	GTTGACCTGG	1500

CTGCGGGCGC CAACATCGCG GGCTTCACCA AGGTGGCTGA TGCCGTCAAG GCCCAGGGCG	1560
CTGTTTAAGC TGCCCAGGCC CAAGCCACGG CTCACCGGCA ATCCAACCCA ACCAACTCAA	1620
CGGCCAGGAC CTTTTCGGAA GCGGCGCCTT TTTCCCAGCC AGGGCCCTCA CCTGCCCTTT	1680
CATAACCCTG CTATTGCCGC CGTGCCCCTG CAATTCCACC CCAAGAAGAA CTAGCGGCAC	1740
TTGACTGCAT CAGGACGGCT ATTTTTTTTCG CGACGCGCGC TCACCCCGAG AGCCTCTCTC	1800
CCCCGAGCCC TAAGCGCTGA CGTCCGCCCCG ACTTTGCCTC GCACATCGCT CGGTTTTGAC	1860
CCCCTCCAGT CTACCCACCC TGTGTGAAG CCTACCAGCT CAATTGCCTT TTAGTGATG	1920
TGCGCCCCCT CCTGCCCCCG AATTTTCCTG CCATGAGACG TGCGGTTTCCT AGCCTGGTGA	1980
CCCCAAGTAG CAGTTAGTGT GCGTGCCTTG CCCTGCGCTG CCCGGGATGC GATACTGTGA	2040
CCTGAGAGTG CTTGTGTAAA CACGACGAGT CAAAAAAAAA AAAAAAAAAA AAAAAA	2096

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATATGGCCG TCTCGCTGGG AGGAG

25

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTTGGATTGC CGGTGAGCC

19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATATGGACG CCACCACCGG C

21

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1506 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 4..1464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAT ATG GCC GTC TCG CTG GAG GAG CAG ATC TCC GCG ATG GAC GCC ACC	48
Met Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr	
515 520 525	

ACC GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG AAG CAG ATG GCC ACC	96
Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala Thr	
530 535 540	

AAG GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC AAG AAC CCC GAC GTG	144
Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp Val	
545 550 555	

CGC CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC CCG GAG CAG CAG GAG	192
Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln Glu	
560 565 570 575	

TTC ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC CTG CAG CCC GTG TTC	240
Phe Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val Phe	
580 585 590	

GAG AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG CAG ATC GTT GAG CCT	288
Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu Pro	
595 600 605	

GAG CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG GAC GAC GCC GGC AAC	336
Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly Asn	
610 615 620	

CTG CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC TCG TCC GCC ATC GGC	384
Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile Gly	
625 630 635	

CCC TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC GTG AAC CTG TCC ATC	432
Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile	
640 645 650 655	

ATG AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG AAC AGC CTG ACC ACC	480
Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr Thr	
660 665 670	
CTG CCC ATG GGC GGC GGC AAG GGC GGC TCC GAC TTC GAC CCC AAG GGC	528
Leu Pro Met Gly Gly Gly Lys Gly Gly Ser Asp Phe Asp Pro Lys Gly	
675 680 685	
AAG AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG TCC TTC ATG ACC GAG	576
Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr Glu	
690 695 700	
CTG CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG CCC GCC GGC GAC ATC	624
Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp Ile	
705 710 715	
GGC GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC GGC CAG TAC AAG CGC	672
Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys Arg	
720 725 730 735	
ATC ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG AAG GGC CAG GAG TAT	720
Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu Tyr	
740 745 750	
GGC GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC TAC GGC GCC GTG CTG	768
Gly Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val Leu	
755 760 765	
TTT GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG AGC CTC AAG GGC AAG	816
Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly Lys	
770 775 780	
CGC TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC CAG TAC TGC GCG GAG	864
Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala Glu	
785 790 795	
CTG CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG CTG TCC GAC TCC CAG	912
Leu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser Gln	
800 805 810 815	

GGC TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC GAG CAG CTG CAG GCG	960
Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln Ala	
820 825 830	
GTG CAG GAC ATG AAG AAG AAG AAC AAC AGC GCC CGC ATC TCC GAG TAC	1008
Val Gln Asp Met Lys Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu Tyr	
835 840 845	
AAG AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC CGC AAG CCT TGG GAG	1056
Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp Glu	
850 855 860	
CTG GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC GCC ACC CAG AAC GAG	1104
Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn Glu	
865 870 875	
ATC GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG CAC GGC TGC CAG TAC	1152
Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln Tyr	
880 885 890 895	
GTG GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC GAG GCC ATC CAC AAG	1200
Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His Lys	
900 905 910	
TAC AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC AAG GCG GCC AAC GCC	1248
Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn Ala	
915 920 925	
GGC GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC CAG AAC CGC ATG AGC	1296
Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met Ser	
930 935 940	
CTG AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG CTG GAG CGC ATC ATG	1344
Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile Met	
945 950 955	
AAG GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC CGC AGA TAC AAT GTT	1392
Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn Val	
960 965 970 975	

GAC CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC ACC AAG GTG GCT GAT 1440
 Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala Asp
 980 985 990

GCC GTC AAG GCC CAG GGC GCT GTT TAAGCTGCCC AGGCCCAAGC CACGGCTCAC 1494
 Ala Val Lys Ala Gln Gly Ala Val
 995

CGGCAATCCA AC 1506

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr Thr
 1 5 10 15

Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala Thr Lys
 20 25 30

Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp Val Arg
 35 40 45

Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln Glu Phe
 50 55 60

Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val Phe Glu
 65 70 75 80

Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu Pro Glu
 85 90 95

Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly Asn Leu
 100 105 110

Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile Gly Pro
 115 120 125

Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile Met
 130 135 140

Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr Thr Leu
 145 150 155 160

Pro Met Gly Gly Gly Lys Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys
 165 170 175

Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr Glu Leu
 180 185 190

Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp Ile Gly
 195 200 205

Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys Arg Ile
 210 215 220

Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu Tyr Gly
 225 230 235 240

Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val Leu Phe
 245 250 255

Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly Lys Arg
 260 265 270

Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala Glu Leu
 275 280 285

Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser Gln Gly
 290 295 300

Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln Ala Val
 305 310 315 320

Gln Asp Met Lys Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu Tyr Lys
 325 330 335

Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp Glu Leu
 340 345 350

Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn Glu Ile
 355 360 365

Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln Tyr Val
 370 375 380

Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His Lys Tyr
 385 390 395 400

Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn Ala Gly
 405 410 415

Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met Ser Leu
 420 425 430

Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile Met Lys
 435 440 445

Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn Val Asp
 450 455 460

Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala Asp Ala
 465 470 475 480

Val Lys Ala Gln Gly Ala Val
 485

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAT ATG GAC GCC ACC ACC GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG	48
Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val	
490 495 500	
 AAG CAG ATG GCC ACC AAG GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC	96
Lys Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile	
505 510 515	
 AAG AAC CCC GAC GTG CGC CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC	144
Lys Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp	
520 525 530	
 CCG GAG CAG CAG GAG TTC ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC	192
Pro Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val Ala Val Ser	
535 540 545 550	
 CTG CAG CCC GTG TTC GAG AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG	240
Leu Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys	
555 560 565	
 CAG ATC GTT GAG CCT GAG CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG	288
Gln Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu	
570 575 580	
 GAC GAC GCC GGC AAC CTG CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC	336

Asp Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr	
585 590 595	
TCG TCC GCC ATC GGC CCC TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC	384
Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser	
600 605 610	
GTG AAC CTG TCC ATC ATG AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG	432
Val Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys	
615 620 625 630	
AAC AGC CTG ACC ACC CTG CCC ATG GGC GGC GGC AAG GGC GGC TCC GAC	480
Asn Ser Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly Gly Ser Asp	
635 640 645	
TTC GAC CCC AAG GGC AAG AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG	528
Phe Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln	
650 655 660	
TCC TTC ATG ACC GAG CTG CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG	576
Ser Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val	
665 670 675	
CCC GCC GGC GAC ATC GGC GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC	624
Pro Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe	
680 685 690	
GGC CAG TAC AAG CGC ATC ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG	672
Gly Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro	
695 700 705 710	
AAG GGC CAG GAG TAT GGC GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC	720
Lys Gly Gln Glu Tyr Gly Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly	
715 720 725	
TAC GGC GCC GTG CTG TTT GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG	768
Tyr Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu	
730 735 740	

AGC CTC AAG GGC AAG CGC TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC	816
Ser Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala	
745 750 755	
CAG TAC TGC GCG GAG CTG CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG	864
Gln Tyr Cys Ala Glu Leu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser	
760 765 770	
CTG TCC GAC TCC CAG GGC TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC	912
Leu Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg	
775 780 785 790	
GAG CAG CTG CAG GCG GTG CAG GAC ATG AAG AAG AAG AAC AAC AGC GCC	960
Glu Gln Leu Gln Ala Val Gln Asp Met Lys Lys Lys Asn Asn Ser Ala	
795 800 805	
CGC ATC TCC GAG TAC AAG AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC	1008
Arg Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg	
810 815 820	
CGC AAG CCT TGG GAG CTG GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC	1056
Arg Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys	
825 830 835	
GCC ACC CAG AAC GAG ATC GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG	1104
Ala Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys	
840 845 850	
CAC GGC TGC CAG TAC GTG GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC	1152
His Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn	
855 860 865 870	
GAG GCC ATC CAC AAG TAC AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC	1200
Glu Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly	
875 880 885	
AAG GCG GCC AAC GCC GGC GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC	1248
Lys Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr	
890 895 900	

CAG AAC CGC ATG AGC CTG AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG	1296
Gln Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys	
905 910 915	
CTG GAG CGC ATC ATG AAG GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC	1344
Leu Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser	
920 925 930	
CGC AGA TAC AAT GTT GAC CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC	1392
Arg Arg Tyr Asn Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe	
935 940 945 950	
ACC AAG GTG GCT GAT GCC GTC AAG GCC CAG GGC GCT GTT TAAGCTGCCC	1441
Thr Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val	
955 960	
AGGCCCAAGC CACGGCTCAC CGGCAATCCA AC	1473

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys	
1 5 10 15	
Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys	
20 25 30	
Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro	
35 40 45	

Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val Ala Val Ser Leu
 50 55 60

Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln
 65 70 75 80

Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp
 85 90 95

Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser
 100 105 110

Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val
 115 120 125

Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn
 130 135 140

Ser Leu Thr Thr Leu Pro Met Gly Gly Gly Lys Gly Gly Ser Asp Phe
 145 150 155 160

Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser
 165 170 175

Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro
 180 185 190

Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly
 195 200 205

Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys
 210 215 220

Gly Gln Glu Tyr Gly Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr
 225 230 235 240

Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser
 245 250 255

Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln
 260 265 270

Tyr Cys Ala Glu Leu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu
 275 280 285

Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu
 290 295 300

Gln Leu Gln Ala Val Gln Asp Met Lys Lys Lys Asn Asn Ser Ala Arg
 305 310 315 320

Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg
 325 330 335

Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala
 340 345 350

Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys His
 355 360 365

Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu
 370 375 380

Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys
 385 390 395 400

Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln
 405 410 415

Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu
 420 425 430

Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg
 435 440 445

Arg Ty r Asn Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr
 450 455 460

Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val
465 470 475